

1645



P#53 1600

RAW SEQUENCE LISTING

DATE: 10/10/2002

PATENT APPLICATION: US/08/325,278B

TIME: 10:34:28

Input Set : D:\402.app.txt

Output Set: N:\CRF4\10102002\H325278B.raw

SEQUENCE LISTING

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 TECH CENTER 1600/2900

ENTERED

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4 (1) GENERAL INFORMATION:
C--> 6 (i) APPLICANT: Bjorck, Lars
7      Sjobring, Ulf
9 (ii) TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
11 (iii) NUMBER OF SEQUENCES: 15
13 (iv) CORRESPONDENCE ADDRESS:
14      (A) ADDRESSEE: Seed IP Law Group
15      (B) STREET: 701 Fifth Avenue Suite 6300
16      (C) CITY: Seattle
17      (D) STATE: Washington
18      (E) COUNTRY: USA
19      (F) ZIP: 98104-7092
21 (v) COMPUTER READABLE FORM:
22      (A) MEDIUM TYPE: Floppy disk
23      (B) COMPUTER: IBM PC compatible
24      (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25      (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27 (vi) CURRENT APPLICATION DATA:
C--> 28      (A) APPLICATION NUMBER: US/08/325,278B
C--> 29      (B) FILING DATE: 26-Oct-1994
30      (C) CLASSIFICATION:
32 (viii) ATTORNEY/AGENT INFORMATION:
33      (A) NAME: Potter, Jane E. R.
34      (B) REGISTRATION NUMBER: 33,332
35      (C) REFERENCE/DOCKET NUMBER: 100084.402
37 (ix) TELECOMMUNICATION INFORMATION:
38      (A) TELEPHONE: (206) 622-4900
39      (B) TELEFAX: (206) 682-6031
42 (2) INFORMATION FOR SEQ ID NO: 1:
44 (i) SEQUENCE CHARACTERISTICS:
45      (A) LENGTH: 305 amino acids
46      (B) TYPE: amino acid
47      (C) STRANDEDNESS: unknown
48      (D) TOPOLOGY: unknown
50 (ii) MOLECULE TYPE: protein
52 (iii) HYPOTHETICAL: NO
54 (vi) ORIGINAL SOURCE:
55      (A) ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
61 Ala Val Glu Asn Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser
62 1 5 10 15
64 Glu Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser

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65          20          25          30
67  Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu
68          35          40          45
70  Ala Tyr Ala Tyr Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr
71          50          55          60
73  Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
74  65          70          75          80
76  Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
77          85          90          95
79  Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
80          100          105          110
82  Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu
83          115          120          125
85  Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
86          130          135          140
88  Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro
89  145          150          155          160
91  Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys
92          165          170          175
94  Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu
95          180          185          190
97  Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Glu Asn Gly Lys Tyr Thr
98          195          200          205
100  Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
101          210          215          220
103  Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
104  225          230          235          240
106  Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
107          245          250          255
109  Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
110          260          265          270
112  Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr
113          275          280          285
115  Thr Ile Asn Ile Arg Phe Ala Gly Lys Lys Val Asp Glu Lys Pro Glu
116          290          295          300
118  Glu
119  305

```

121 (2) INFORMATION FOR SEQ ID NO: 2:

122 (i) SEQUENCE CHARACTERISTICS:

123 (A) LENGTH: 921 base pairs

124 (B) TYPE: nucleic acid

125 (C) STRANDEDNESS: double

126 (D) TOPOLOGY: unknown

127 (ii) MOLECULE TYPE: DNA (genomic)

128 (iii) HYPOTHETICAL: NO

129 (vi) ORIGINAL SOURCE:

130 (A) ORGANISM: Escherichia coli LE392/pHDL, DSM 7054

131 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

132 GCGGTAGAAA ATAAAGAAGA AACACCAGAA ACACCAGAAA CTGATTCAGA AGAAGAAGTA

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142 ACAATCAAAG CTAACCTAAT CTTTGCAAAT GGAAGCACAC AAACCTGCAGA ATTCAAAGGA 120
144 ACATTTGAAA AAGCAACATC AGAAGCTTAT GCGTATGCAG ATACTTTGAA GAAAGACAAT 180
146 GGAGAAATATA CTGTAGATGT TGCAGATAAA GGTTATACTT TAAATATTAA ATTTGCTGGA 240
148 AAAGAAAAAA CACCAGAAGA ACCAAAAGAA GAAGTTACTA TTAAAGCAAA CTTAATCTAT 300
150 GCAGATGGAA AAACACAAAC AGCAGAATTC AAAGGAACAT TTGAAGAAGC AACAGCAGAA 360
152 GCATACAGAT ATGCAGATGC ATTAAGAAG GACAATGGAG AATATACAGT AGACGTTGCA 420
154 GATAAAGGTT ATACTTTAAA TATTAAATTT GCTGGAAAAG AAAAAACACC AGAAGAACCA 480
156 AAAGAAGAAG TTACTATTAA AGCAAACTTA ATCTATGCAG ATGGAAAAAC ACAAACAGCA 540
158 GAATTCAAAG GAACATTTGA AGAAGCAACA GCAGAAGCAT ACAGATATGC TGAATTATTA 600
160 GCAAAAGAAA ATGGTAAATA TACAGTAGAC GTTGCAGATA AAGGTTATAC TTTAAATATT 660
162 AAATTTGCTG GAAAAGAAAA AACACCAGAA GAACCAAAAAG AAGAAGTTAC TATTAAAGCA 720
164 AACTTAATCT ATGCAGATGG AAAAACTCAA ACAGCAGAGT TCAAAGGAAC ATTTGCAGAA 780
166 GCAACAGCAG AAGCATAACG ATACGCTGAC TTATTAGCAA AAGAAAATGG TAAATATACA 840
168 GCAGACTTAG AAGATGGTGG ATACACTATT AATATTAGAT TTGCAGGTAA GAAAGTTGAC 900
170 GAAAAACCAG AAGAATAATA A
921

```

172 (2) INFORMATION FOR SEQ ID NO: 3:

174 (i) SEQUENCE CHARACTERISTICS:

175 (A) LENGTH: 434 amino acids

176 (B) TYPE: amino acid

177 (C) STRANDEDNESS: unknown

178 (D) TOPOLOGY: unknown

180 (ii) MOLECULE TYPE: protein

182 (iii) HYPOTHETICAL: NO

184 (vi) ORIGINAL SOURCE:

185 (A) ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055

189 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

191 Ala Val Glu Asn Lys Glu Glu Thr Pro Glu Thr Asp Ser
192 1 5 10 15
194 Glu Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser
195 20 25 30
197 Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu
198 35 40 45
200 Ala Tyr Ala Tyr Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr
201 50 55 60
203 Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
204 65 70 75 80
206 Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
207 85 90 95
209 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
210 100 105 110
212 Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu
213 115 120 125
215 Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
216 130 135 140
218 Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro
219 145 150 155 160
221 Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys
222 165 170 175
224 Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu

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```

225          180          185          190
227 Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Glu Asn Gly Lys Tyr Thr
228          195          200          205
230 Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
231          210          215          220
233 Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
234          225          230          235          240
236 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
237          245          250          255
239 Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
240          260          265          270
242 Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr
243          275          280          285
245 Thr Ile Asn Ile Arg Phe Ala Gly Lys Lys Val Asp Glu Lys Pro Glu
246          290          295          300
248 Glu Pro Met Asp Thr Tyr Lys Leu Ile Leu Asn Gly Lys Thr Leu Lys
249          305          310          315          320
251 Gly Glu Thr Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys Val
252          325          330          335
254 Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr
255          340          345          350
257 Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Lys Pro Glu Val Ile
258          355          360          365
260 Asp Ala Ser Glu Leu Thr Pro Ala Val Thr Thr Tyr Lys Leu Val Ile
261          370          375          380
263 Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr Thr Lys Ala Val Asp Ala
264          385          390          395          400
266 Glu Thr Ala Glu Lys Ala Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val
267          405          410          415
269 Asp Gly Val Trp Thr Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val Thr
270          420          425          430
272 Glu Met

```

275 (2) INFORMATION FOR SEQ ID NO: 4:

277 (i) SEQUENCE CHARACTERISTICS:

278 (A) LENGTH: 1308 base pairs

279 (B) TYPE: nucleic acid

280 (C) STRANDEDNESS: double

281 (D) TOPOLOGY: unknown

283 (ii) MOLECULE TYPE: DNA (genomic)

285 (iii) HYPOTHETICAL: NO

287 (vi) ORIGINAL SOURCE:

288 (A) ORGANISM: Escherichia coli L392/pHDLG, DSM 7055

292 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

294 GCGGTAGAAA ATAAAGAAGA AACACCAGAA ACACCAGAAA CTGATTCAGA AGAAGAAGTA      60
296 ACAATCAAAG CTAACCTAAT CTTTGCAAAT GGAAGCACAC AAATGCAGA ATTCAAAGGA      120
298 ACATTTGAAA AAGCAACATC AGAAGCTTAT GCGTATGCAG ATACTTTGAA GAAAGACAAT      180
300 GGAGAATATA CTGTAGATGT TGCAGATAAA GGTATACTTT TAAATATTAA ATTTGCTGGA      240
302 AAAGAAAAAA CACCAGAAGA ACCAAAAGAA GAAGTTACTA TTAAAGCAAA CTTAATCTAT      300
304 GCAGATGGAA AAACACAAAC AGCAGAATTC AAAGGAACAT TTGAAGAAGC AACAGCAGAA      360

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306 GCATACAGAT ATGCAGATGC ATTAAAGAAG GACAAATGGAG AATATACAGT AGACGTTGCA      420
308 GATAAAGGTT ATACTTTAAA TATTAAATTT GCTGGAAAAG AAAAAACACC AGAAGAACCA      480
310 AAAGAAGAAG TTACTATTAA AGCAAACTTA ATCTATGCAG ATGGAAAAAC ACAAAACAGCA      540
312 GAATTCAAAG GAACATTTGA AGAAGCAACA GCAGAAAGCAT ACAGATATGC TGACTTATTA      600
314 GCAAAAGAAA ATGGTAAATA TACAGTAGAC GTTGCAGATA AAGGTTATAC TTAAATATT      660
316 AAATTTGCTG GAAAAGAAAA AACACCAGAA GAACCAAAAG AAGAAGTTAC TATTAAAGCA      720
318 AACTTAATCT ATGCAGATGG AAAAAGCTCA ACAGCAGAGT TCAAAGGAAC ATTTGCAGAA      780
320 GCAACAGCAG AAGCATACAG ATACGCTGAC TTATTAGCAA AAGAAAATGG TAAATATACA      840
322 GCAGACTTAG AAGATGGTGG ATACACTATT AATATTAGAT TTGCAGGTAA GAAAGTTGAC      900
324 GAAAAACCAAG AAGAACCCAT GGACACTTAC AAATTAATCC TTAATGGTAA AACATTGAAA      960
326 GCGGAAACAA CTACTGAAGC TGTGTATGCT GCTACTGCAG AAAAAGTCTT CAAACAATAC     1020
328 GCTAACGACA ACGGTGTTGA CGGTGAATGG ACTTACGACG ATGCGACTAA GACCTTTACA     1080
330 GTTACTGAAA AACCAGAAGT GATCGATGCG TCTGAATTAA CACCAGCCGT GACAACCTAC     1140
332 AAACCTGTGA TTAATGGTAA AACATTGAAA GGCGAAACAA CTACTAAAGC AGTAGACGCA     1200
334 GAAACTGCAG AAAAAGCCTT CAAACAATAC GCTAACGACA ACGGTGTTGA TGGTGTGTTG     1260
336 ACTTATGATG ATGCGACTAA GACCTTTACG GTAACGTAAA TGTAATAA      1308
338 (2) INFORMATION FOR SEQ ID NO: 5:
340     (i) SEQUENCE CHARACTERISTICS:
341         (A) LENGTH: 1332 base pairs
342         (B) TYPE: nucleic acid
343         (C) STRANDEDNESS: double
344         (D) TOPOLOGY: unknown
346     (ii) MOLECULE TYPE: DNA (genomic)
348     (iii) HYPOTHETICAL: NO
351     (ix) FEATURE:
352         (A) NAME/KEY: CDS
353         (B) LOCATION: 1..1329
356     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
358 AAC GGT GAT GGT AAT CCT AGG GAA GTT ATA GAA GAT CTT GCA GCA AAC      48
359 Asn Gly Asp Gly Asn Pro Arg Glu Val Ile Glu Asp Leu Ala Ala Asn
360   1           5           10           15
362 AAT CCC GCA ATA CAA AAT ATA CGT TTA CGT CAC GAA AAC AAG GAC TTA      96
363 Asn Pro Ala Ile Gln Asn Ile Arg Leu Arg His Glu Asn Lys Asp Leu
364           20           25           30
366 AAA GCG AGA TTA GAG AAT GCA ATG GAA GTT GCA GGA AGA GAT TTT AAG     144
367 Lys Ala Arg Leu Glu Asn Ala Met Glu Val Ala Gly Arg Asp Phe Lys
368           35           40           45
370 AGA GCT GAA GAA CTT GAA AAA GCA AAA CAA GCC TTA GAA GAC CAG CGT     192
371 Arg Ala Glu Glu Leu Glu Lys Ala Lys Gln Ala Leu Glu Asp Gln Arg
372           50           55           60
374 AAA GAT TTA GAA ACT AAA TTA AAA GAA CTA CAA CAA GAC TAT GAC TTA     240
375 Lys Asp Leu Glu Thr Lys Leu Lys Glu Leu Gln Gln Asp Tyr Asp Leu
376   65           70           75           80
378 GCA AAG GAA TCA ACA AGT TGG GAT AGA CAA AGA CTT GAA AAA GAG TTA     288
379 Ala Lys Glu Ser Thr Ser Trp Asp Arg Gln Arg Leu Glu Lys Glu Leu
380           85           90           95
382 GAA GAG AAA AAG GAA GCT CTT GAA TTA GCG ATA GAC CAG GCA AGT CGG     336
383 Glu Glu Lys Lys Glu Ala Leu Glu Leu Ala Ile Asp Gln Ala Ser Arg
384           100           105           110

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VERIFICATION SUMMARY

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Input Set : D:\402.app.txt

Output Set: N:\CRF4\10102002\H325278B.raw

L:6 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:]
L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]